What is Claimed is:

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1. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotypes shown in the table immediately below defines one copy of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on at least one copy of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	10	PS	PS	Haj	plotyp	e Num	ber(c)	(Part 1	.)				
		No.(a)	Position(b)	1	2	3	4	5	6	7	8	9	10
ļ-i		1	504	G	G	G	G	G	G	G	G	G	G
		2	717	\boldsymbol{C}	C	C	C	C	C	C	C	С	C
C.		3	744	G	G	G	G	G	G	G	G	G	G
	15	4	778	С	C	C	C	С	С	С	T	T	T
ağını atrıs		5	1009	C	C	G	G	G	G	G	C	C	C
Ø		6	1045	C	C	T	T	T	T	T	C	C	C
222 F		7	1122	G	G	Α	G	G	G	G	G	G	G
		8	1218	С	C	C	C ·	C	C	C	Α	Α	С
≘	20	9	2014	С	C	C	C	C	C	T	C	C	C
		10	2177	T	T	. T	T	T	T	C	T	T	T
		11	5906	C	T	T	C	T	T	T	С	T	C
		12	6010	С	C	C	C	C	T	T	С	C	C
W.		13	8110	G	G	G	G	G	G	G	G	G	G
D.	25	14	8333	С	C	C	C	C	C	T	C	C	С
ΠIJ		15	8354	Α	Α	Α	Α	Α	Α	Α	G	Α	Α
		16	8402	Α	Α	Α	Α	Α	\mathbf{A}	G	Α	Α	A
		17	8459	Α	Α	Α	A	Α	Α	Α	Α	Α	Α
		18	10203	G	G	G	G	G	G	G	G	G	G
	30	19	10512	T	T	С	T	T	T	T	T	T	T

		PS	PS	Har	olotype	e Numi	ber(c)	(Part 2	2)				
		No.(a)	Position(b)	11	12	13	14	15	16	17	18	19	20
		1	504	G	G	G	G	G	G	G	G	G	G
	5	2	717	C	C	C	C	C	C	C	C	C	C
		3	744	G	G	ر G	Ġ	G	G	G	G	G	T
		4	778	T	T	T	T	T	T	T	T	T	Ţ
		5 .	1009	C	C	G	G	G	G	G	G	G	G
		6	1045	С	C	C	C	C	C	C'	C	C	C
	10	. 7	1122	G	G	G	G	G	G ·	G	G	G	G
		8	1218	С	C	Α	Α	Α	C	C	C	C	C
		9	2014	С	T	С	C	С	C	C	C	C	C
		10	2177	T	C	T	T	T	T	T	T	T	T
		11	5906	T	T	C	T	T	C	T	T	T	T
	15	12	6010	C	C	C	С	C	C	C	C	C	C
<u> -</u>		13	8110	G	G	Α	G	G	G	A	G	G	G
		14	8333	С	С	C	C	C	C	C	C	C	C
		15	8354	Α	Α	Α	Α	A	Α	A	A	A	A
4		16	8402	Α	G	Α	Α	A	A	A	A	A	A
=	20	17	8459	Α	C	A	Α	A	A	A	A	A	A
<u> </u>		18	10203	Α	G	G	G	G	G	G	G	G	G
1121 2 ⁴²¹ 1		19	10512	T	T	C	С	T	T	T	C	T	T
uğu Em					_			~	• `				
≅ .====		PS	PS			e Num	ber(c)	(Part	3)				
<u></u>	25	No.(a)	Position(b)	21	22								
		1	504	G	T								
닖		2	717	T	C					•			
ű m		3	744	G	G								
C		4	778	C	T								
IW	30	5	1009	C ·	G								
		6	1045	C	C								
		7	1122	G	G								
		8	1218	C	C								
		9	2014	C	C								
	35	10	2177	T	T								
		11	5906	C C	T C								
		12	6010										
		13	8110	G C	A C						_		
	40	14	8333										
	40	15	8354	A	A								
		16	8402	A	A								
		17	8459	A	A								
		18	10203	G T	G C			•					
	45	19	10512	1	C								
	45		_										

(a) PS = polymorphic site;
(b) Position of PS within SEQ ID NO:1;
(c) Alleles for haplotypes are presented 5' to 3' in each column.

2. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises determining which of the TNFRSF11B haplotype pairs shown in the table immediately below defines both copies of the individual's TNFRSF11B gene, wherein the determining step comprises identifying the phased sequence of nucleotides present at each of PS1-PS19 on both copies of the individual's TNFRSF11B gene, and wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions and identities are set forth in the table immediately below:

	10	PS	PS	Hap	lotype P	Pair(c) (P	art 1)				
٠,		No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
10		1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
1m 1m2		3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	15	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
T		5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
1		6 .	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
100 m		7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
e Cj	20	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	· C/C	C/C
<u>lu</u>		10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
		11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
		12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
		13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	25	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
i tu		15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
		16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
		17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
		18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	30	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

		PS	PS	Hap	lotype P	air(c) (F	Part 2)				
		No.(a)	Position(b)	.10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
		1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		2	717	C/C	C/C	C/C	· C/C	C/T	C/C	C/C	C/C
	5	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
		5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
		6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/T	· C/T
		7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	10	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
		9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
		10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
		11	5906	C/T	T/T	· T/C	T/T	C/C	T/T	T/T	C/T
		12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	15	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
h		14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
		15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
		16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
- म्यूनिय राग		17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	20	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
C٦		19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
, F 1											
B		PS	PS	_	lotype F			/-		40.00	10/10
	25	PS No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
	25	No.(a)	Position(b) 504	1/2 G/G	19/4 G/G	19/3 G/G	19/9 G/G	G/G	G/G	G/G	G/G
	25	No.(a) 1 2	Position(b) 504 717	1/2 G/G C/C	19/4 G/G C/C	19/3 G/G C/C	19/9 G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C
	25	No.(a) 1 2 3	Position(b) 504 717 744	1/2 G/G C/C G/G	19/4 G/G C/C G/G	19/3 G/G C/C G/G	19/9 G/G C/C G/G	G/G C/C G/G	G/G C/C G/T	G/G C/C G/G	G/G C/C G/G
		No.(a) 1 2 3 4	Position(b) 504 717 744 778	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C	19/3 G/G C/C G/G T/C	19/9 G/G C/C G/G T/T	G/G C/C G/G T/C	G/G C/C G/T T/T	G/G C/C G/G T/C	G/G C/C G/G T/T
	25 30	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C G/G	19/3 G/G C/C G/G T/C G/G	19/9 G/G C/C G/G T/T G/C	G/G C/C G/G T/C G/G	G/G C/C G/T T/T G/G	G/G C/C G/G T/C G/G	G/G C/C G/G T/T G/G
		No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	1/2 G/G C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T	19/3 G/G C/C G/G T/C G/G C/T	19/9 G/G C/C G/G T/T G/C C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/T T/T G/G C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/G T/T G/G C/C
		No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	1/2 G/G C/C G/G C/C C/C C/C G/G	19/4 G/G C/C G/G T/C G/G C/T G/G	19/3 G/G C/C G/G T/C G/G C/T G/A	19/9 G/G C/C G/G T/T G/C C/C G/G	G/G C/C G/G T/C G/G C/T G/A	G/G C/C G/T T/T G/G C/C G/G	G/G C/C G/G T/C G/G C/T G/G	G/G C/C G/G T/T G/G C/C G/G
		No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	1/2 G/G C/C G/G C/C C/C C/C G/G C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A	G/G C/C G/G T/C G/G C/T G/A A/C	G/G C/C G/T T/T G/G C/C G/G	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
	30	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	1/2 G/G C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C	G/G C/C G/T T/T G/G C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
		No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	1/2 G/G C/C G/G C/C C/C C/C C/C T/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C	G/G C/C G/G T/C G/G C/T G/G C/C C/T	G/G C/C G/G T/T G/G C/C G/G C/C C/C
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	1/2 G/G C/C G/G C/C C/C C/C C/C T/T C/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C	G/G C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	1/2 G/G C/C G/G C/C C/C C/C G/G C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T C/C	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T	G/G C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	1/2 G/G C/C G/G C/C C/C C/C T/T C/C G/G	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T G/G	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	1/2 G/G C/C G/G C/C C/C C/C C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/C T/T C/T G/G C/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	1/2 G/G C/C G/G C/C C/C C/C C/C C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	1/2 G/G C/C G/G C/C C/C G/G C/C C/C T/T C/C G/G C/C A/A A/A	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/T T/C T/T C/T G/G C/T A/A A/G	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459 10203	1/2 G/G C/C G/G C/C C/C G/G C/C C/C T/T C/C G/G C/C A/A A/A A/A	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C T/T T/T C/C G/G C/C A/A A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A A/A	G/G C/C G/G T/C G/G C/T T/C T/T C/T G/G C/T A/A A/G A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A A/A
	30	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	1/2 G/G C/C G/G C/C C/C G/G C/C C/C T/T C/C G/G C/C A/A A/A	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/T T/C T/T C/T G/G C/T A/A A/G	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A

		PS	PS		lotype P	air(c) (F					
		No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
		1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	5	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
		4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
		5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
		6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
		7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	10	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
		9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
		10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
		11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
		12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
ļai. pag		14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
		15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
[m]		16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
्राष्ट्र सर्वा		17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	20	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	.G/G	G/G
H:		19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T
		PS	PS	Har	olotype F	Pair(c) (I	Part 5)				
Ξ.		No.(a)	Position(b)	3/14) F		,				
	25	1	504	G/G							
		2	717	C/C				•			
		3	744	G/G							
L.		4	778	C/T							
		5	1009	G/G							
TU	30	6	1045	T/C							
		7	1122	A/G							•
		8	1218	C/A							
		9	2014	C/C							
		10	2177	T/T							
	35	11	5906	T/T							
		12	6010	C/C							
		13,	8110	G/G							
		14	8333	C/C							
		15	8354	A/A							
	40	16	8402	A/A							
		17	8459	A/A							
		18	10203	G/G	•						•
٠		19	10512	C/C							

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⁽a) PS = polymorphic site;
(b) Position of PS in SEQ ID NO:1;
(c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column.

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- 3. A method for genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, comprising determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at one or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the one or more polymorphic sites (PS) have the position and alternative alleles shown in SEQ ID NO:1.
- 4. The method of claim 3, wherein the determining step comprises:
 - (a) isolating from the individual a nucleic acid mixture comprising both copies of the TNFRSF11B gene, or a fragment thereof, that are present in the individual;
 - (b) amplifying from the nucleic acid mixture a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for genotyping the selected polymorphic site in the target region;
 - (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
- 5. The method of claim 3, which comprises determining for the two copies of the TNFRSF11B gene present in the individual the identity of the nucleotide pair at each of PS1-PS19.
- 6. A method for haplotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual which comprises determining, for one copy of the TNFRSF11B gene present in the individual, the identity of the nucleotide at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 7. The method of claim 6, further comprising determining the identity of the nucleotide at PS5, wherein the PS has the position and alternative alleles shown in SEQ ID NO:1.
- 8. The method of claim 6, wherein the determining step comprises:
 - (a) isolating from the individual a nucleic acid sample containing only one of the two copies of the TNFRSF11B gene, or a fragment thereof, that is present in the individual;
 - (b) amplifying from the nucleic acid sample a target region containing one of the selected polymorphic sites;
 - (c) hybridizing a primer extension oligonucleotide to one allele of the amplified target region, wherein the oligonucleotide is designed for haplotyping the selected polymorphic site in

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the target region;

- (d) performing a nucleic acid template-dependent, primer extension reaction on the hybridized oligonucleotide in the presence of at least one terminator of the reaction, wherein the terminator is complementary to one of the alternative nucleotides present at the selected polymorphic site; and
 - (e) detecting the presence and identity of the terminator in the extended oligonucleotide.
 - 9. A method for predicting a haplotype pair for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual comprising:
 - identifying a TNFRSF11B genotype for the individual, wherein the genotype comprises the nucleotide pair at two or more polymorphic sites (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1;
 - (b) comparing the genotype to the haplotype pair data set forth in the table immediately below; and
 - (c) determining which haplotype pair is consistent with the genotype of the individual and with the haplotype pair data

	PS	PS	Hap	olotype F	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
15	1.	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2 ·	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	. T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
20	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
*	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	.9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
25 -	11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	8110	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
30	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

35	PS	PS	Hap	lotype P	air(c) (F					
	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
40	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
	6	1045	C/C	C/C	, C/C	C/C	C/C	C/C	C/T	C/T
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
45	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	13	8110	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
50	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	_ A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
55	19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
	PS	PS .		lotype I						
	PS No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
	No.(a) 1	Position(b) 504	1/2 G/G	19/4 G/G	19/3 G/G	19/9 G/G	G/G	G/G	G/G	G/G
60	No.(a) 1 2	Position(b)	1/2 G/G C/C	19/4 G/G C/C	19/3 G/G C/C	19/9 G/G C/C	G/G C/C	G/G C/C	G/G C/C	G/G C/C
60	No.(a) 1 2 3	Position(b) 504 717 744	1/2 G/G C/C G/G	19/4 G/G C/C G/G	19/3 G/G C/C G/G	19/9 G/G C/C G/G	G/G C/C G/G	G/G C/C G/T	G/G C/C G/G	G/G C/C G/G
60	No.(a) 1 2 3 4	Position(b) 504 717 744 778	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C	19/3 G/G C/C G/G T/C	19/9 G/G C/C G/G T/T	G/G C/C G/G T/C	G/G C/C G/T T/T	G/G C/C G/G T/C	G/G C/C G/G T/T
60	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C G/G	19/3 G/G C/C G/G T/C G/G	19/9 G/G C/C G/G T/T G/C	G/G C/C G/G T/C G/G	G/G C/C G/T T/T G/G	G/G C/C G/G T/C G/G	G/G C/C G/G T/T G/G
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	1/2 G/G C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T	19/3 G/G C/C G/G T/C G/G C/T	19/9 G/G C/C G/G T/T G/C C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/T T/T G/G C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/G T/T G/G C/C
60	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	1/2 G/G C/C G/G C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G	19/3 G/G C/C G/G T/C G/G C/T G/A	19/9 G/G C/C G/G T/T G/C C/C G/G	G/G C/C G/G T/C G/G C/T G/A	G/G C/C G/T T/T G/G C/C G/G	G/G C/C G/G T/C G/G C/T G/G	G/G C/C G/G T/T G/G C/C G/G
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	1/2 G/G C/C G/G C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A	G/G C/C G/G T/C G/G C/T G/A A/C	G/G C/C G/T T/T G/G C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	1/2 G/G C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C	G/G C/C G/T T/T G/G C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	1/2 G/G C/C G/G C/C C/C C/C C/C T/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C	G/G C/C G/G T/C G/G C/T G/G C/C C/T	G/G C/C G/G T/T G/G C/C G/G C/C C/C
65	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	1/2 G/G C/C G/G C/C C/C C/C C/C T/T C/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T
	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	1/2 G/G C/C G/G C/C C/C C/C C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T	G/G C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T
65	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C T/T C/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G
65	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	1/2 G/G C/C G/G C/C C/C C/C C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
65	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	1/2 G/G C/C G/G C/C C/C C/C C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A
70	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A A/G	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
65	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A A/G A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
70	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A A/G	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A

	PS	PS	Hap	lotype P	air(c) (F	Part 4)				
80	No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16
•	1.	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T
85	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
•	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C
90	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T
	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	13	. 8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
95	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T
100										
100										
100	PS	PS		lotype P	air(c) (I	Part 5)				
100	PS No.(a)	PS Position(b)	3/14	lotype P	air(c) (I	Part 5)				
100	No.(a)	Position(b) 504	3/14 G/G	lotype P	air(c) (I	Part 5)				
	No.(a) 1 2	Position(b) 504 717	3/14 G/G C/C	lotype P	'air(c) (I	Part 5)				
100	No.(a) 1 2 3	Position(b) 504 717 744	3/14 G/G C/C G/G	lotype P	'air(c) (I	Part 5)				
	No.(a) 1 2 3 4	Position(b) 504 717 744 778	3/14 G/G C/C G/G C/T	lotype P	'air(c) (I	Part 5)				
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	3/14 G/G C/C G/G C/T G/G	lotype P	'air(c) (I	Part 5)				
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	3/14 G/G C/C G/G C/T G/G T/C	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	3/14 G/G C/C G/G C/T G/G T/C A/G	lotype P	'air(c) (I	Part 5)				
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	3/14 G/G C/C G/G C/T G/G T/C A/G C/A	lotype P	'air(c) (I	art 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	'air(c) (I	Part 5)				
105 110 115	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	'air(c) (I	Part 5)				
105	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	lotype P	'air(c) (I	Part 5)				

- (a) PS = polymorphic site;
- (b) Position of PS in SEQ ID NO:1;
- (c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column.
 - 10. The method of claim 9, wherein the identified genotype of the individual comprises the nucleotide pair at each of PS1-PS19, which have the position and alternative alleles shown in SEQ ID NO:1.
 - 11. A method for identifying an association between a trait and at least one haplotype or haplotype

pair of the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)

(TNFRSF11B) gene which comprises comparing the frequency of the haplotype or haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype pair in a reference population, wherein the haplotype is selected from haplotypes 1-22 shown in the table presented immediately below, wherein each of the haplotypes comprises a sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

PS PS Haplotype Number(c) (Part 1) No.(a) Position(b) 1 2 3 4 5 6 7 8 9 1 504 G G G G G G G G G 15 2 717 C C C C C C C C C 3 744 G G G G G G G G G 4 778 C C C C C C C C C T T	10 G C
1 504 G G G G G G G G G G G G G G G G G G G	
3 744 G G G G G G G G G G G G G G G G G G	C
4 778 C C C C C C T T	
	T
5 1009 C C G G G C C	C
6 1045 C C T T T T C C	
20 7 1122 G G A G G G G G	
8 1218 C C C C C C A A	
9 2014 C C C C C C T C C	
10 2177 T T T T T C . T T	T
11 5906 C T T C T T C T	C
25 12 6010 C C C C C T T C C	
13 8110 G G G G G G G	
14 8333 C C C C C C T C C	
15 8354 A · A A A A A G A	
16 8402 A A A A A A G A A	
30 17 8459 A A A A A A A A	
18 10203 G G G G G G G	
19 10512 T T C T T T T T	T
PS PS Haplotype Number(c) (Part 2)	
35 No.(a) Position(b) 11 12 13 14 15 16 17 18 19	20
1 504 G G G G G G G	
2 717 C C C C C C C C	
3 · 744 G G G G G G G	
4 778 T T T T T T T T	
40 5 1009 C C G G G G G	
6 1045 C C C C C C C C	
7 1122 G G G G G G G	
8 1218 C C A A A C C C C	
9 2014 C T C C C C C C	
45 10 2177 T C T T T T T T	T
11 5906 T T C T T C T T T	T
12 6010 C C C C C C C C	
13 8110 G G A G G A G G	
14 8333 C C C C C C C C	C
50 15 8354 A A A A A A A A	
16 8402 A G A A A A A A	
17 8459 A C A A A A A A	
18 10203 A G G G G G G	
19 10512 T T C C T T T C T	1

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	PS	PS	Haj	plotype	e Number(c) (Part 3)
	No.(a)	Position(b)	21	22	
	1	504	G	T	
60	2	717	T	C	
	3	744	G	G	
	4	778	С	T	
	5	1009	С	G	
	. 6	1045	Ç	С	
65	7	1122	Ğ	G	
	8	1218	C	C	
	9	2014	C	C	
	10	2177	T	T	•
•	11	5906	C	T	
70	12	6010	C	С	
	13	8110	G	Α	•
	14	8333	С	C	
	15	8354	Α	Α	•
	16	8402	Α	Α	
75	17	8459	Α	Α	
	18	10203	G	G	
	19	10512	T	C	

- (a) PS = polymorphic site;
- (b) Position of PS within SEQ ID NO:1;
 - (c) Alleles for haplotypes are presented 5' to 3' in each column;

and wherein the haplotype pair is selected from the haplotype pairs shown in the table immediately below, wherein each of the TNFRSF11B haplotype pairs consists of first and second haplotypes which comprise first and second sequences of polymorphisms whose positions in SEQ ID NO:1 and identities are set forth in the table immediately below:

	PS	PS	Hap	lotype P	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
90	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
95	7.	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177	T/T	T/T	T/T	T/T	C/C	T/T	T/T	T/T
	11 .	5906	C/C	T/T	T/T	T/T	Ţ/T	T/C	C/T	C/T
100	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	.8110	G/G	G/G	G/G	G/G	G/G	G/G·	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
•	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
105	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T ,	T/T	T/T	T/T	T/T	T/T	T/T

	PS	PS	Hap	lotype F	air(c) (I	Part 2)				
110	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G						
	2	717	C/C	C/C	C/C	C/C	C/T	C/C	C/C	C/C
	3	744	G/G	G/G						
	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C
115	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G	C/G
	6	1045	C/C	C/C	C/C	C/C	·C/C	C/C	C/T	C/T
	7	1122	G/G	G/G						
	8	1218	C/A	C/A	C/A	A/C	C/C	C/C	A/C	C/C
100	9	2014	C/C	C/C	C/C	C/T	C/C	C/C	C/C	C/C
120	10	2177	T/T	T/T	T/T	T/C	T/T	T/T	T/T	T/T
	11	5906	C/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C G/G	C/T	C/T G/G
	13 14	8110 8333	G/G C/C	G/G C/C	G/A C/C	G/G C/C	G/G C/C	C/C	. G/G C/C	C/C
125	15	8354	A/A	A/A						
125	16	8402	A/A A/A	A/A	A/A	A/G	A/A A/A	A/A A/A	A/A	A/A
	17	8459	A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
	19	10512	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
130	• •	10012	1.0	2. 0	2, 0			-/-		
	PS	PS	Hap	lotype F	air(c) (I	Part 3)				
,	No.(a)	Position(b)	1/2	19/4	19/3	19/9	15/3	19/20	19/7	19/18
	1	504	G/G	G/G						
	2	717	C/C	C/C						
135	3	744	G/G	G/G	G/G	G/G	G/G	G/T	G/G	G/G
	4	778	C/C	T/C	T/C	T/T	T/C	T/T	T/C	T/T
	5	1009	C/C	G/G	G/G	G/C	G/G	G/G	G/G	G/G
	6	1045	C/C	C/T	C/T	C/C	C/T	C/C	C/T	C/C
	7	1122	G/G	G/G	G/A	G/G	G/A	G/G	G/G	G/G
140	8	1218	C/C	C/C	C/C	C/A	A/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	C/C T/T	C/C T/T	C/T T/C	C/C T/T
	10	2177 5906	T/T C/T	T/T T/C	T/T T/T	T/T T/T	T/T	T/T	T/T	T/T
	11 12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
145	13	8110	G/G	G/G	G/G	· G/G	G/G	G/G	G/G	G/G
140.	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/C
	15	8354	A/A	A/A						
	16	8402	A/A	A/A	A/A	A/A	A/A	A/A	A/G	A/A
	17	8459	A/A	A/A						
150	18	10203	G/G	G/G						
-50	19	10512	T/T	T/T	T/C	T/T	T/C	T/T	T/T	T/C

	PS	PS	Hap	lotype P	air(c) (I	Part 4)					
	No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16	
155	1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	2	· 717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	3	· 744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	4	778 ´	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T	
	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G	
160	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C	
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C	
	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T	
165	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C	
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A	
170	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A	
	17	8459	A/A	A/C	A/C	A/A	A/A	A/A	A/A	A/A	
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T	
•	17	10312	O/ I	1/1	1/1			-/-	1/1		
175							• 1, •	27.2			
175	PS	PS	Hap	lotype P			**,*	1/1			
175	PS No.(a)	PS Position(b)	Hap 3/14				**,*				
175	PS No.(a)	PS Position(b) 504	Hap 3/14 G/G				**,*				
175	PS No.(a) 1 2	PS Position(b) 504 717	Hap 3/14 G/G C/C				**,*				
	PS No.(a) 1 2 3	PS Position(b) 504 717 744	Hap 3/14 G/G C/C G/G				•,•				
175 180	PS No.(a) 1 2 3 4	PS Position(b) 504 717 744 778	Hap 3/14 G/G C/C G/G C/T				• 0				
	PS No.(a) 1 2 3 4 5	PS Position(b) 504 717 744 778 1009	Hap 3/14 G/G C/C G/G C/T G/G				• , •	• •			
	PS No.(a) 1 2 3 4	PS Position(b) 504 717 744 778	Hap 3/14 G/G C/C G/G C/T				• 7,-				
	PS No.(a) 1 2 3 4 5 6	PS Position(b) 504 717 744 778 1009 1045	Hap 3/14 G/G C/C G/G C/T G/G T/C				• 0				
	PS No.(a) 1 2 3 4 5 6 7	PS Position(b) 504 717 744 778 1009 1045 1122	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G								
180	PS No.(a) 1 2 3 4 5 6 7 8	PS Position(b) 504 717 744 778 1009 1045 1122 1218	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A								
180	PS No.(a) 1 2 3 4 5 6 7 8	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A				• •				
180	PS No.(a) 1 2 3 4 5 6 7 8 9	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A								
180	PS No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Hap 3/14 G/G C/C G/G C/T G/G T/C A/G C/A C/C T/T T/T C/C G/G C/C A/A A/A								

⁽a) PS = polymorphic site;

wherein a higher frequency of the haplotype or haplotype pair in the trait population than in the reference population indicates the trait is associated with the haplotype or haplotype pair.

12. The method of claim 11, wherein the trait is a clinical response to a drug targeting TNFRSF11B or to a drug for treating a condition or disease predicted to be associated with TNFRSF11B

⁽b) Position of PS in SEQ ID NO:1;

⁽c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column;

- activity.
- 13. An isolated oligonucleotide designed for detecting a polymorphism in the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene at a polymorphic site (PS) selected from the group consisting of PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 14. The isolated oligonucleotide of claim 13, which is an allele-specific oligonucleotide that specifically hybridizes to an allele of the TNFRSF11B gene at a region containing the polymorphic site.
- 15. The allele-specific oligonucleotide of claim 14, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:4-21, the complements of SEQ ID NOS:4-21, and SEQ ID NOS:22-57.
- 16. The isolated oligonucleotide of claim 13, which is a primer-extension oligonucleotide.
- 17. The primer-extension oligonucleotide of claim 16, which comprises a nucleotide sequence selected from the group consisting of SEQ ID NOS:58-93.
- 18. A kit for haplotyping or genotyping the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) gene of an individual, which comprises a set of oligonucleotides designed to haplotype or genotype each of polymorphic sites (PS) PS1, PS2, PS3, PS4, PS6, PS7, PS8, PS9, PS10, PS11, PS12, PS13, PS14, PS15, PS16, PS17, PS18 and PS19, wherein the selected PS have the position and alternative alleles shown in SEQ ID NO:1.
- 19. The kit of claim 18, which further comprises oligonucleotides designed to genotype or haplotype PS5, wherein the selected PS has the position and alternative alleles shown in SEQ ID NO:1.
- 20. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
 - (a) a first nucleotide sequence which comprises a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the TNFRSF11B isogene is selected from the group consisting of isogenes 1- 18 and 20 22 shown in the table immediately below and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1- 18 and 20 22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below; and

Region	PS	PS	Iso	gene N	lumber	r(d) (P	art 1)					
Examined(a)	No.(b)	Position(c)	1	.2	3	4	5	6	7	8	9	10
427-1437	1	504	G	G	G	G	G	G	G	G	G	G
427-1437	2	717	С	C	C	C	C	С	C	С	С	C
427-1437	3	744	G	G	G	G	G	G	G	G	G	G
427-1437	4	778	С	С	С	С	C	С	C	T	T	T
427-1437	5	1009	С	С	G	G	G	G	G	C	С	C
427-1437	6	1045	С	C	T	T	\mathbf{T}	T	T	C	C	С
427-1437	7	1122	G	G	Α	G	G	G	G	G	G	G
427-1437	8	1218	С	С	C	C	С	C	C	Α	Α	C
1604-2208	9	2014	С	C	C	С	C	С	T	C	C	С
1604-2208	10	2177	T	T	T	T	T	T	C	T	T	T
5748-6485	11	5906	С	T	T	. C	T	T	T	C	T	. C
5748-6485	12	6010	С	C	С	C	C	T	T	С	C	C
8035-8653	13	8110	G	G	G	G	G	G.	G	G	G	G
8035-8653	14	8333	С	C	C	С	C	C	T	C	C	C
8035-8653	15	8354	Α	Α	Α	Α	Α	Α	Α	G	Α	Α
8035-8653	16	8402	Α	Α	Α	Α	Α	Α	G	Α	Α	Α
8035-8653	17	8459	Α	Α	Α	Α	Α	Α	Α	Α	Α	Α
9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
	. 19	10512	T	T	С	T	T	T	T	T	T	T
9942-10628	19	10312	•	•	•					•		
	PS	PS		gene N			art 2)					
9942-10628 Region Examined(a)	PS						art 2)	16	17	18	20	
Region	PS	PS	Iso	gene N	Jumbe	r(d) (P 14 G		G	G	G	G	
Region Examined(a)	PS No.(b)	PS Position(c)	Iso 11	gene N 12	Jumber 13	r(d) (P 14	15		G C	G C	G C	
Region Examined(a) 427-1437	PS No.(b)	PS Position(c) 504	Iso 11 G	gene N 12 G C C	Jumber 13 G	r(d) (P 14 G	15 G	G C G	G C G	G C G	G C T	
Region Examined(a) 427-1437 427-1437	PS No.(b) 1 2	PS Position(c) 504 717	Iso 11 G C G T	gene N 12 G C G T	Jumber 13 G C G T	r(d) (P 14 G C G T	15 G C G T	G C G T	G C G T	G C G T	G C T T	
Region Examined(a) 427-1437 427-1437	PS No.(b) 1 2 3 4 5	PS Position(c) 504 717 744 778 1009	Iso 11 G C G T C	gene N 12 G C G T C	Jumber 13 G C G T G	r(d) (P 14 G C G T G	15 G C G T G	G C G T G	G C G T G	G C G T G	G C T T G	
Region Examined(a) 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5 6	PS Position(c) 504 717 744 778 1009 1045	Iso 11 G C G T C	gene N 12 G C G T C	Jumber 13 G C G T G	r(d) (P 14 G C G T G	15 G C G T G	G C G T G C	G C G T G C	G C G T G	G C T T G C	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5 6 7	PS Position(c) 504 717 744 778 1009 1045 1122	Iso 11 G C G T C C	gene N 12 G C G T C C G	Iumber 13 G C G T G C	r(d) (P 14 G C G T G C	15 G C G T G	G C G T G C G	G C G T G C G	G C G T G C	G C T G C G	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	PS No.(b) 1 2 3 4 5 6 7 8	PS Position(c) 504 717 744 778 1009 1045 1122 1218	Iso 11 G C G T C C G	gene N 12 G C G T C G C C	Iumber 13 G C G T G C G	r(d) (P 14 G C G T G C G	15 G C G T G C G	G C G C G C	G C G T G C G	G C G T G C G	G C T T G C G	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208	PS No.(b) 1 2 3 4 5 6 7 8	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014	Iso 11 G C G T C C C C C	gene N 12 G C G T C C G T	Jumber 13 G C G T G C G A	r(d) (P 14 G C G T G C G A C	G C G C G A C	G C G C C C	G C G C C C	G C G T G C G C	G C T T G C G C	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208	PS No.(b) 1 2 3 4 5 6 7 8	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177	Iso 11 G C G T C C C C T	gene N 12 G C G T C C G C T C	Jumber 13 G C G T G C G A C	r(d) (P 14 G C G T G C G A C	15 G C G T G C G A C	G C G C C C C	G C G T G C G C C T	G C G T G C G C C	G C T G C G C C	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485	PS No.(b) 1 2 3 4 5 6 7 8 9 10	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	Iso 11 G C G T C C C T T	gene N 12 G C G T C C G T T T	Jumber 13 G C G T G C T C	r(d) (P 14 G C G T G C G A C	G C G C G A C T T	G C G C C T C	G C G C C C T T	G C G C C T T	G C T T G C G C T T	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	Iso 11 G C G T C C C C T T C	gene N 12 G C G T C C G T C C C T C	Jumber 13 G C G T G C G A C T C	r(d) (P 14 G C G T G C G A C T T	G C G C C T T C C	G C G T G C G C T C C	G C G C C C T T C	G C G C C T T C	G C T T G C G C T T C	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	Iso 11 G C G T C C C T T C G G T	gene N 12 G C G T C C G T C G C T C G G	Jumber 13 G C G T G C G A C T C	r(d) (P 14 G C G T G C G A C T T C G	G C G A C T T C G	G C G T G C G C C T C C G	G C G C G C C T T C A	G C G T G C C T T C G	G C T T G C G C C T T C G	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	Iso 11 G C G T C C C T T C C C C C C C C C C C	gene N 12 G C G T C C G T C C C C C C C C C C C C	Jumber 13 G C G T G C G A C T C C	r(d) (P 14 G C G T G C G A C T T C G	G C G A C T T C G C	GCGTGCGCCTCCGC	G C G T G C C T T C A C	G C G T G C C T T C G C	G C T T G C G C C T T C G C	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	Iso 11 G C G T C C G C T T C G C A	gene N 12 G C G T C C G C T C T C A	Jumber 13 G C G T G C G A C T C C A	r(d) (P 14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C A	G C G T G C G C C T C C G C A	G C G C C T T C A C A	G C G C C T T C G C A	G C T T G C G C C T T C G C A	· ·
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Iso 11 G C G T C C G C T T C G A A	gene N 12 G C G T C C G C T C C G C A G	Jumber 13 G C G T G C G A C C A C A	r(d) (P 14 G C G T G C G A C T T C G C A A	G C G A C T T C G C A A	G C G T G C G C A A	G C G C C C T T C A C A	G C G C C T T C G C A A	G C T T G C G C C T T C G C A A	
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	Iso 11 G C G C C T T C G C A A A A	gene N 12 G C G T C C G C T C T C G C A G C	Jumber 13 G C G T G C G A C T C C A C A A	r(d) (P 14 G C G T G C G A C T T C G C A A A	G C G A C T T C G C A A A	G C G T G C G C A A A	G C G C C T T C A C A A A	G C G T G C C T T C G C A A A	G C T T G C G C C T T C G C A A A	:
Region Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653	PS No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	PS Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	Iso 11 G C G T C C G C T T C G A A	gene N 12 G C G T C C G C T C C G C A G	Jumber 13 G C G T G C G A C C A C A	r(d) (P 14 G C G T G C G A C T T C G C A A	G C G A C T T C G C A A	G C G T G C G C A A	G C G C C C T T C A C A	G C G C C T T C G C A A	G C T T G C G C C T T C G C A A	:

Region	PS	PS	Iso	gene N	Number(d) (Part 3)
Examined(a)	No.(b)	Position(c)	21	22	
427-1437	I	504	G	T	
427-1437	2	717	T	С	
427-1437	3	. 744	G	G	
427-1437	4	778	C	T	
427-1437	5	1009	C	G	
427-1437	6	1045	. C	C	
427-1437	7	1122	G	G	
427-1437	8	1218	C	C	
1604-2208	9	2014	C	C	
1604-2208	10	2177	T	T _.	
5748-6485	11	5906	C	T	
5748-6485	12	6010	С	С	
8035-8653	13	8110	G	Α	
8035-8653	14	8333	С	С	
8035-8653	15	8354	Α	Α	
8035-8653	16	8402	Α	Α	
8035-8653	17	8459	Α	Α	
9942-10628	18	10203	G	G	
9942-10628	19	10512	T	С	

- (a) Region examined represents the nucleotide positions defining the start and stop positions within the 1st SEQ ID NO of the sequenced region;
- (b) PS = polymorphic site;
- (c) Position of PS in SEQ ID NO:1;
- (d) Alleles for isogenes are presented 5' to 3' in each column;
- (b) a second nucleotide sequence which is complementary to the first nucleotide sequence.
- 21. The isolated polynucleotide of claim 20, which is a DNA molecule and comprises both the first and second nucleotide sequences and further comprises expression regulatory elements operably linked to the first nucleotide sequence.
- 22. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 21, wherein the organism expresses a TNFRSF11B protein that is encoded by the first nucleotide sequence.
- 23. The recombinant nonhuman organism of claim 22, which is a transgenic animal.
- An isolated fragment of a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) isogene, wherein the fragment comprises at least 10 nucleotides in one of the regions of SEQ ID NO:1 shown in the table immediately below and wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at PS1, thymine at PS2, thymine at PS3, cytosine at PS4, thymine at PS6, adenine at PS7, adenine at PS8, thymine at PS9, cytosine at PS10, cytosine at PS11, thymine at PS12, adenine at PS13, thymine at PS14, guanine at PS15, guanine at PS16, cytosine at PS17, adenine at PS18 and cytosine at PS19, wherein the selected polymorphism has the position set forth in the table immediately below:

10													
·	Region	PS	PS	Iso	gene N	Iumbe	r(d) (Pa	art 1)					
	Examined(a)	No.(b)	Position(c)	1	. 2	3	4	5	6	7.	8	9	10
	427-1437	1	504	G	G	G	G	G	G	G	G	G	G
	427-1437	2	717	С	С	C	С	С	C	С	С	С	C
15	427-1437	3	744	G	G	G	G	G	G	G	G	G	G
	427-1437	4	778	C	С	С	С	С	С	С	T	Т	T
	427-1437	5	1009	С	C	G	G	G	G	G	С	C	С
	427-1437	6	1045	С	С	T	T	T	T	Τ.	С	C	С
	427-1437	7	1122	G	G	Α	G	G	G.	G	G	G	G
- 20	427-1437	8	1218	С	С	С	С	С	C	C	Α	Α	С
	1604-2208	9	2014	С	С	С	C	С	С	T	C	С	С
	1604-2208	10	2177	T	T	T	T	Т	T	С	T	Т	T
	5748-6485	11	5906	C	T	T	C	T	T	T	С	T	С
	5748-6485	12	6010	C	·C	C	C	С	T	T	С	С	С
25	8035-8653	13	8110	Ğ	G	Ğ	G	G	G	G	G	G	G
	8035-8653	14	8333	Č	Č	Č	Č	Č	Č	T	Č	Č	Ċ
	8035-8653	15	8354	Ā	Ā	Ā	Ā	Ā	Ā	Ā	G	Ā	A
	8035-8653	16	8402	A	A	A	A	A	A	G	Ā	A	A
	8035-8653	17	8459	A	A	A	A	A	A	Ā	A	A	A
30	9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
	9942-10628	19	10512	Ť	Ť	Č	T	Ť	Ť	T	Ť	Ť	T
))	.,	10512	•	-	•	•	-	•	-	•	-	_
	Region	PS,	PS	Iso	gene N	Jumbe	r(d) (P	art 2)					
	Examined(a)		Position(c)	11	12	13	14	15	16	17	18	20	
35	427-1437	1	504	G	G	G	G	G	G	G	G	G	
	427-1437	2	717	C	C	Č	C	C	C	C	C	С	
	427-1437	3	744	G	G	Ğ	Ğ	Ğ	Ğ	G	G	T	
	427-1437	4	778	T	T	T	Ť	Ť	T	T	T	T	
	427-1437	5	1009	Ĉ	C	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	
40	427-1437	6	1045	Č	Č	Č	Č	Č	Č	Č	Č	C	
	427-1437	7	1122	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	G	G	G	
	427-1437	8	1218	Č	Č	Ā	Ä	Ā	Č	Č	Č	C	
	1604-2208	9	2014	Č	Ť	C	C	C	Č	Č	C	Č	
	1604-2208	10	2177	Ť	Ĉ	Ť	Ť	Ť	Ť	Ť	Ť	Ť	
45	5748-6485	11	5906	Ť	Ť	Ċ	T.	T.	Ĉ	T	T	T	
15	5748-6485	12	6010	Ĉ	Ĉ	Č	Ĉ	Ċ	Č	Ĉ	Ĉ	Ĉ	
•	8035-8653	13	8110	Ğ	Ğ	Ă	·Ğ	Ğ	Ğ	Ă	Ğ	Ğ	
	8035-8653	14	8333	Č	Č	C	Č	Č	Č	C	Č	Č	
	8035-8653	15	8354	Ä	Ă	Ä	Ă	Ä	Ă	Ä	Ă	Ă	
50	8035-8653	16	8402	A	G	A	A	A	A	A	A	A	
50	8035-8653	17	8459	A	Ċ	A	A	A	A	A	A	A	
	9942-10628	18	10203	A	G	G	G	Ğ	Ğ	G	Ğ	G	
	9942-10628	19	10203	T.	T	C	C	T	T	T	C	·T	
	フプサム・11/07/8	17	10312	1	1	•	U	1	ı		U		

55	Region	PS	PS	Iso	gene Number(d) (Part 3)
	Examined(a)	No.(b)	Position(c)	21	22
-	427-1437	1	504	G	T
	427-1437	2	717	T	C
	427-1437	3	744	G	G
60	427-1437	4	778	C	T
	427-1437	5	1009	C	G
	427-1437	6	1045	C	C
	427-1437	7	1122	G	G
	427-1437	8	1218	C	C
65	1604-2208	9	2014	C	C
	1604-2208	10	2177	T	T
	5748-6485	11	5906	C	T
	5748-6485	12	6010	С	C
	8035-8653	13	8110	G	A
70	8035-8653	14	8333	С	C
	8035-8653	15	8354	Α	A
	8035-8653	16	8402	Α	Α
	8035-8653	17	8459	Α	A
	9942-10628	18	10203	G	G
75	9942-10628	19	10512	T	C

- (a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
- (b) PS = polymorphic site;
- (c) Position of PS within SEQ ID NO:1;
 - (d) Alleles for TNFRSF11B isogenes are presented 5' to 3' in each column.
- 25. An isolated polynucleotide comprising a coding sequence for a TNFRSF11B isogene, wherein the coding sequence comprises SEQ ID NO:2, except at each of the polymorphic sites which have the positions in SEQ ID NO:2 and polymorphisms set forth in the table immediately below:

PS	PS	Isoge	ene Codi	ing Se	quence	Numl	er(c)	(Part 1)		
No.(a)	Position(b)	1c	2c	3c	7c	8c	9c	10c	11c	12c	13c
5	9	C	C	G	G	C	C	C	C	C	G
14	699	С	C	C	T	C	С	С	C	C	C
15	720	Α	Α	Α	Α	G	Α	Α	Α	Α	Α
16	768	Α	Α	Α	G	Α	Α	Α	Α	G	Α
18	841	G	G	G	G	G	G	G	Α	G	G
19	1150	T	T	С	T	T	T	T	T	T	C
PS	PS	Isoge	ene Cod	ing Se	quence	Numl	per(c)	(Part 2)		
No.(a)	Position(b)	14c	18c	21c	22c						
5	9	G	G	С	G						
14	699	С	С	С	C						
15	720	Α	Α	Α	Α						
16	768	Α	Α	Α	Α						
18	841	G	G	G	G						
19	1150	С	С	Т	C						

- (a) PS = polymorphic site;
- (b) Position of PS in SEQ ID NO:2;
- (c) Alleles for the isogene coding sequence are presented 5' to 3' in each column; the numerical

- portion of the isogene coding sequence number represents the number of the parent full TNFRSF11B isogene.
- 26. A recombinant nonhuman organism transformed or transfected with the isolated polynucleotide of claim 25, wherein the organism expresses a tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein that is encoded by the polymorphic variant sequence.
- 27. The recombinant nonhuman organism of claim 26, which is a transgenic animal.
- 28. An isolated fragment of a TNFRSF11B coding sequence, wherein the fragment comprises one or more polymorphisms selected from the group consisting of thymine at a position corresponding to nucleotide 699, guanine at a position corresponding to nucleotide 720, guanine at a position corresponding to nucleotide 841 and cytosine at a position corresponding to nucleotide 1150 in SEQ ID NO:2.
- An isolated polypeptide comprising an amino acid sequence which is a polymorphic variant of a reference sequence for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) (TNFRSF11B) protein, wherein the reference sequence comprises SEQ ID NO:3, except the polymorphic variant comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281.
- An isolated monoclonal antibody specific for and immunoreactive with the isolated polypeptide of claim 29.
- 31. A method for screening for drugs targeting the isolated polypeptide of claim 29 which comprises contacting the TNFRSF11B polymorphic variant with a candidate agent and assaying for binding activity.
- 32. An isolated fragment of a TNFRSF11B protein, wherein the fragment comprises one or more variant amino acids selected from the group consisting of methionine at a position corresponding to amino acid position 240 and methionine at a position corresponding to amino acid position 281 in SEQ ID NO:3.
- 33. A computer system for storing and analyzing polymorphism data for the tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin) gene, comprising:
 - (a) a central processing unit (CPU);
 - (b) a communication interface;
 - (c) a display device;

- (d) an input device; and
- (e) a database containing the polymorphism data; wherein the polymorphism data comprises the haplotypes set forth in the table immediately below:

10	PS	PS	Hap	lotype	Numb	er(c) ((Part 1))				
	No.(a)	Position(b)	1	2 .	3	4	5	6	7	8	9	10
	I	504	G	G	G	G	G	G	G	G	G C	G C
	2	717	C	C	C	C	C	C	C G	C G	G	G
	3	744	G	G	G	G C	G C	G C	C	T	T	T
15	4	778	C	C	C G	G	G	G	G	Ċ	Ċ	Ċ
	5	1009	C	C	T	T.	T	T	T	Ċ	Č.	Č
	, 6	1045	C	C G	A	G	Ğ	G	Ğ	Ğ	G	Ğ
	7	1122 1218	G C	C	C	C	C	C	Ċ	A	A	c
20	8 9	2014	C	C	Ċ	Č	Č	č	T	C	C	Č
20	9 10	2014	T	T	T	T	T	T	Ċ	Ť	Ť	Ť
	11	5906	Ċ	Ť	T	Ċ	Ť	Ť	T.	Ĉ	T	Ċ
	12	6010	Č	Ċ	Ĉ	č	Ĉ	Ť	T	Č	C	C
	13	8110	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ.	Ğ	G	G
25	13	8333	Č	Č	Č	Č	Ĉ	Č	T	C	C	С
23	15	8354	Ā	Ā	Ā	A	Α	Α	Α	G	Α	Α
	16	8402	A	A	Α	Α	Α	Α	G	Α	Α	Α
	17	8459	A	Α	Α	Α	Α	Α	Α	Α	Α	Α
	18	10203	G	G	G	G	G	G	G	G	G	G
30	19	10512	T	T	C	T	T	T	Т	T	T	T
	PS	PS	Ha	plotyp	e Num	ber(c)	(Part 2	2)				
	PS No.(a)	PS Position(b)	Ha:	12	13	14	15	16	17	18	19	20
		Position(b) 504	11 G	12 G	13 G	14 G	15 G	16 G	G	G	G	G
35	No.(a) 1 2	Position(b) 504 717	11 G C	12 G C	13 G C	14 G C	15 G C	16 G C	G C	G C	G C	G C
35	No.(a) 1 2 3	Position(b) 504 717 744	11 G C G	12 G C G	13 G C G	14 G C G	15 G C G	16 G C G	G C G	G C G	G C G	G C T
35	No.(a) 1 2 3 4	Position(b) 504 717 744 778	11 G C G T	12 G C G T	13 G C G T	14 G C G T	15 G C G T	16 G C G T	G C G T	G C G T	G C G T	G C T T
35	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009	G C G T C	12 G C G T	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G	G C G T G	G C G T G	G C T T G
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	11 G C G T C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	16 G C G T G	G C G T G	G C G T G	G C G T G C	G C T G C
35	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	G G T C G	12 G C G T C C	13 G C G T G C	14 G C G T G C	15 G C G T G C	16 G C G T G C	G C G T G C	G C G T G C	G C G T G C	G T T G C
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	G C C C C C	12 G C G T C C G	13 G C G T G C G	14 G C G T G C G A	15 G C G T G C G	16 G C G T G C G	G C G T G C G	G G T G C G	G G T G C G	G T T G C G C
	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	11 G C G T C C G C	12 G C G T C C G C	G C G C G A C	14 G C G T G C G A C	G C G C G A C	16 G C G T G C G C	G G T G C G C	G G T G C G C	G G T G C G C	G C T T G C G C C
	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	G C C C C T	12 G C G T C C G C T	13 G C G T G C G A C	14 G C G T G C G A C	15 G C G T G C G A C	16 G C G T G C G C C	G C G C C T	G C G T G C G C T	G C G T G C G C	G C T T G C G C C T
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	G C C C C T T	12 G C G T C C G C T C T	G C G C G A C T C	14 G C G T G C G A C T	G C G C G A C T T	16 G C G T G C C T C	G C G C C T T	G C G C C T T	G C G T G C C C T T	G C T T G C G C C T T
	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	G C C C C T T C	12 G C G T C C G C T C T C	G C G C G A C T C C	14 G C G T G C G A C T T C	15 G C G T G C G A C T T	16 G C G T G C G C C T C C	G C G T G C C T T C	G C G T G C C T T C	G C G T G C G C C T T C	G C T T G C G C C T T C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	G C C C C T T C G	12 G C G T C C G C T C G G	G C G C C C C A	14 G C G T G C G A C T T C G	15 G C G T G C G A C T T C G	16 G C G C C T C C G	G C G T G C G C C T T C A	G C G T G C G C C T T C G	G C G T G C G C C T T C G	G C T T G C G C C T T C G
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	G C C C T T C G C	G C G C T C C G C	G C G A C T C C A C	14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C	16 G C G T G C C C T C C G C	G C G T G C G C C T T C A C	G C G T G C G C C T T C G C	G C G T G C G C C T T C	G C T T G C G C C T T C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	G C C C C T T C G C A	12 G C G T C C G C T C T C G C A	13 G C G T G C G A C T C C A C A	14 G C G T G C G A C T T C G C A	G C G A C T T C G C A	16 G C G T G C G C C T C C G C A	G C G T G C C T T C A C A	G C G T G C G C T T C G C A	G C G T G C G C C T T C G C	G C T T G C G C C T T C G C
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	G C C C C T T C G C A A	12 G C G T C C G C T C G C A G	13 G C G T G C G A C T C C A C A A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	16 G C G T G C G C C A A	G C G T G C G C C T T C A C	G C G T G C G C C T T C G C	G C G T G C G C T T C G C A	G C T T G C G C C T T C G C A
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	G C C C C C C C A A A	12 G C G T C C G C T C T C G C A G C	13 G C G T G C G A C T C C A C A A A	14 G C G T G C G A C T T C G C A A A	15 G C G T G C G A C T T C G C A A A	16 G C G T G C G C C T C C G C A	G C G T G C G C T T C A C A A	G C G T G C G C T T C G C A A	G C G T G C G C T T C G C A A	G C T T G C G C C T T C G C A A A G
40	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	G C C C C T T C G C A A	12 G C G T C C G C T C G C A G	13 G C G T G C G A C T C C A C A A	14 G C G T G C G A C T T C G C A A	15 G C G T G C G A C T T C G C A A	16 G C G T G C G C C A A A	G C G T G C G C T T C A C A A A	G C G T G C G C T T C G C A A A	G C G T G C G C T T C G C A A A	G C T T G C G C C T T C G C A A A

	PS	PS	Ha	plotyp	e Number(c) (Part 3)
55	No.(a)	Position(b)	21	22	
	1	504	G	T	
	2	717 -	T	C	•
	3	744	G	G	
	4	778	С	T	
60	5	1009	С	G	
	6	1045	C	C	
	7	1122	G	G	
	8	1218.	С	C	
	9	2014	C	C	
65	10	2177	Т	T	
	11	5906	С	T	•
	12	6010	С	C	
	13	8110	G	Α	
	14	8333	С	C	
70	15	8354	Α	Α	
	16	8402	Α	Α	
	17	8459	Α	Α	
	18	10203	G	G	
	19	10512	T	С	•
75					

- (a) PS = polymorphic site;
 (b) Position of PS within SEQ ID NO:1;
 (c) Alleles for haplotypes are presented 5' to 3' in each column;

80 the haplotype pairs set forth in the table immediately below:

	PS	PS	Hap	lotype F	air(c) (P	art 1)				
	No.(a)	Position(b)	1/1	15/15	19/19	6/6	12/12	19/16	10/2	1/5
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
85	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	4	778	C/C	T/T	T/T	C/C	T/T	T/T	T/C	C/C
	5	1009	C/C	G/G	G/G	G/G	C/C	G/G	C/C	C/G
	6	1045	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/T
90	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	8	1218	C/C	A/A	C/C	C/C	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C	C/C	C/C	T/T	C/C	C/C	C/C
	10	2177		T/T	T/T	T/T	C/C	T/T	T/T	T/T
	11	5906	C/C	T/T	T/T	T/T	T/T	T/C	C/T	C/T
95	12	6010	C/C	C/C	C/C	T/T	C/C	C/C	C/C	C/C
	13	8110	· G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
	15	8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
	16	8402	A/A	A/A	A/A	A/A	G/G	A/A	A/A	A/A
100	17	8459	A/A	A/A	A/A	A/A	C/C	A/A	A/A	A/A
	18	- 10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	19	10512	T/T	T/T	T/T	T/T	T/T	T/T	T/T	T/T

	PS	PS			air(c) (F					
105	No.(a)	Position(b)	10/14	19/14	19/13	15/12	1/21	19/11	15/6	1/6
	1	504	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G
	2	717	C/C	C/C	C/C	C/C .		C/C	C/C	C/C
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G C/C
	4	778	T/T	T/T	T/T	T/T	C/C	T/T	T/C	C/C C/G
110	5	1009	C/G	G/G	G/G	G/C	C/C	G/C	G/G C/T	C/G C/T
	6	1045	C/C	C/C	C/C	C/C	C/C	C/C G/G	G/G	G/G
	7	1122	G/G	G/G		G/G A/C	G/G C/C	C/C	A/C	C/C
	8	1218	C/A	C/A	C/A C/C	C/T	C/C	C/C	C/C	C/C
	9	2014	C/C	C/C T/T	T/T	T/C	T/T	T/T	T/T	T/T
115	10	2177	T/T	T/T	T/C	T/T	C/C	T/T	T/T	C/T
	11	5906	C/T C/C	C/C	C/C	C/C	C/C	C/C	C/T	C/T
	12	6010	G/G	G/G	G/A	G/G	G/G	G/G	G/G	G/G
	13	8110	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C
120	14	8333 8354	A/A	A/A	A/A	A/A	A/A	A/A	A/A	A/A
120	15 16	8334 8402	A/A A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A
	17	8459	, A/A	A/A	A/A	A/C	A/A	A/A	A/A	A/A
	18	10203	G/G	G/G	G/G	G/G	G/G	G/A	G/G	G/G
	19	10203	T/C	T/C	T/C	T/T	T/T	T/T	T/T	T/T
105	17	10312	1,0	210						
125										
125	PS	PS	Har	olotype l	Pair(c) (Part 3)				
125	PS No.(a)	PS Position(b)	Har 1/2	olotype l 19/4	Pair(c) (1 19/3	Part 3) 19/9	15/3	19/20	19/7	19/18
125	PS No.(a)	PS Position(b) 504				Part 3) 19/9 G/G	15/3 G/G	19/20 G/G	G/G	G/G
125	No.(a) 1	Position(b)	1/2	19/4	19/3	19/9	G/G C/C	G/G C/C	G/G C/C	G/G C/C
130	No.(a)	Position(b) 504	1/2 G/G	19/4 G/G C/C G/G	19/3 G/G C/C G/G	19/9 G/G C/C G/G	G/G C/C G/G	G/G C/C G/T	G/G C/C G/G	G/G C/C G/G
	No.(a) 1 2 3 4	Position(b) 504 717	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C	19/3 G/G C/C G/G T/C	19/9 G/G C/C G/G T/T	G/G C/C G/G T/C	G/G C/C G/T T/T	G/G C/C G/G T/C	G/G C/C G/G T/T
	No.(a) 1 2 3 4 5	Position(b) 504 717 744	1/2 G/G C/C G/G C/C	19/4 G/G C/C G/G T/C G/G	19/3 G/G C/C G/G T/C G/G	19/9 G/G C/C G/G T/T G/C	G/G C/C G/G T/C G/G	G/G C/C G/T T/T G/G	G/G C/C G/G T/C G/G	G/G C/C G/G T/T G/G
	No.(a) 1 2 3 4 5	Position(b) 504 717 744 778 1009 1045	1/2 G/G C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T	19/3 G/G C/C G/G T/C G/G C/T	19/9 G/G C/C G/G T/T G/C C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/T T/T G/G C/C	G/G C/C G/G T/C G/G C/T	G/G C/C G/G T/T G/G C/C
130	No.(a) 1 2 3 4 5 6 7	Position(b) 504 717 744 778 1009 1045 1122	1/2 G/G C/C G/G C/C C/C C/C G/G	19/4 G/G C/C G/G T/C G/G C/T G/G	19/3 G/G C/C G/G T/C G/G C/T G/A	19/9 G/G C/C G/G T/T G/C C/C G/G	G/G C/C G/G T/C G/G C/T G/A	G/G C/C G/T T/T G/G C/C G/G	G/G C/C G/G T/C G/G C/T G/G	G/G C/C G/G T/T G/G C/C G/G
	No.(a) 1 2 3 4 5 6 7 8	Position(b) 504 717 744 778 1009 1045 1122 1218	1/2 G/G C/C G/G C/C C/C C/C G/G C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A	G/G C/C G/G T/C G/G C/T G/A A/C	G/G C/C G/T T/T G/G C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
130	No.(a) 1 2 3 4 5 6 7 8 9	Position(b) 504 717 744 778 1009 1045 1122 1218 2014	1/2 G/G C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C	G/G C/C G/T T/T G/G C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C	G/G C/C G/G T/T G/G C/C G/G C/C
130	No.(a) 1 2 3 4 5 6 7 8 9 10	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177	1/2 G/G C/C G/G C/C C/C C/C C/C T/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C	G/G C/C G/G T/T G/G C/C G/G C/C C/C
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	1/2 G/G C/C G/G C/C C/C C/C G/G C/C T/T C/T	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C	G/G C/C G/G T/T G/G C/C G/G C/C C/C T/T T/T
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	1/2 G/G C/C G/G C/C C/C C/C G/G C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T	G/G C/C G/T T/T G/G C/C G/G C/C C/C T/T T/T	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	1/2 G/G C/C G/G C/C C/C C/C C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G	G/G C/C G/G T/C G/G C/T G/G C/C C/T T/C T/T C/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	1/2 G/G C/C G/G C/C C/C G/G C/C C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C C/C T/T T/C C/C G/G C/C	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C T/T G/G C/T	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	1/2 G/G C/C G/G C/C C/C G/G C/C C/C G/G C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C	G/G C/C G/G T/C G/G C/T G/G C/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/T T/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
130 135 140	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/T T/C T/T C/T G/G C/T A/A A/G A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A
130	No.(a) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(b) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	1/2 G/G C/C G/G C/C C/C G/G C/C C/C C/C C/C	19/4 G/G C/C G/G T/C G/G C/T G/G C/C T/T T/C C/C G/G C/C A/A A/A	19/3 G/G C/C G/G T/C G/G C/T G/A C/C C/C T/T T/T C/C G/G C/C A/A A/A	19/9 G/G C/C G/G T/T G/C C/C G/G C/A C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/A A/C C/C T/T T/T C/C G/G C/C A/A	G/G C/C G/T T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A	G/G C/C G/G T/C G/G C/T G/G C/T T/C T/T C/T G/G C/T A/A	G/G C/C G/G T/T G/G C/C G/G C/C T/T T/T C/C G/G C/C A/A A/A

	PS	PS	Han	lotype P	air(c) (I	Part 4)					
	No.(a)	Position(b)	22/17	19/12	1/12	19/8	15/10	19/15	19/10	18/16	
150	1	504	T/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	2	717	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	3	744	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	4	778	T/T	T/T	C/T	T/T	T/T	T/T	T/T	T/T	
	5	1009	G/G	G/C	C/C	G/C	G/C	G/G	G/C	G/G	
155	6	1045	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
_	7	1122	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
•	8	1218	C/C	C/C	C/C	C/A	A/C	C/A	C/C	C/C	
	9	2014	C/C	C/T	C/T	C/C	C/C	C/C	C/C	C/C	
	10	2177	T/T	T/C	T/C	T/T	T/T	T/T	T/T	T/T	
160	11	5906	T/T	T/T	C/T	T/C	T/C	T/T	T/C	T/C	
	12	6010	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	13	8110	A/A	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	14	8333	C/C	C/C	C/C	C/C	C/C	C/C	C/C	C/C	
	15	8354	A/A	A/A	A/A	A/G	A/A	A/A	A/A	A/A	
165	16	8402	A/A	A/G	A/G	A/A	A/A	A/A	A/A	A/A	
	17	8459	A/A	A/C	A/C	À/A	A/A	A/A	A/A	A/A	
	18	10203	G/G	G/G	G/G	G/G	G/G	G/G	G/G	G/G	
	19	10512	C/T	T/T	T/T	T/T	T/T	T/T	T/T	C/T	
170	PS	PS	Han	lotype P	air(c) (I	Part 5)					
	No.(a)	Position(b)	3/14		(-) (-	,					
	1	504	G/G								
	2	717	C/C					•			
	3	744	G/G								
175	4	778	C/T								
	5	1009	G/G								
	6	1045	T/C								
	7	1122	A/G								
	8 .	1218	C/A								
180	9	2014	C/C								
	10	. 2177	T/T								
	11	5906	T/T					•			
	12	6010	C/C								
	13	8110	G/G								
185	14	8333	C/C								
	15	8354	A/A								
	16	8402	A/A								
	17	8459	A/A								
	18	10203	G/G								
190	19	10512	C/C								
		(a) PS = poly	mornhic	site:							
		(b) Position of			NO:1;						•

A genome anthology for the tumor necrosis factor receptor superfamily, member 11b 34. (osteoprotegerin) (TNFRSF11B) gene which comprises two or more TNFRSF11B isogenes

⁽b) Position of PS in SEQ ID NO:1; (c) Haplotype pairs are represented as 1st haplotype/2nd haplotype; with alleles of each haplotype shown 5' to 3' as 1st polymorphism/2nd polymorphism in each column;

or the frequency data in Tables 6 and 7.

selected from the group consisting of isogenes 1-22 shown in the table immediately below, and wherein each of the isogenes comprises the regions of SEQ ID NO:1 shown in the table immediately below and wherein each of the isogenes 1-22 is further defined by the corresponding sequence of polymorphisms whose positions and identities are set forth in the table immediately below:

	Region	PS	PS	Isc	gene l	Numbe	r(d) (F	art 1)	,	1			
10	Examined(a)	No.(b)	Position(c)	1	2	3	4	5	6	7	8	9	10
	427-1437	1	504 `	G	G	G	G	G	Ğ	Ğ	Ğ	Ġ	Ğ
	427-1437	. 2	717	C	C	Č	Č	Č	Č	Č	Č	Č	Č
	427-1437	3	744	G	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ
	427-1437	4	778	Ċ	Č	Č	Č	Č	Č	Č	T	T.	T
15	427-1437	5	1009	Č	Č	Ğ	Ğ	Ğ	Ğ	Ğ	Ĉ	Ċ	Ċ
	427-1437	6	1045	Č	Č	T	T	T	T	T	Č	Č	Č
	427-1437	7	1122	Ğ	Ğ	Ā	Ġ	Ġ	Ğ	Ġ	Ğ	Ğ	Ğ
	427-1437	8	1218	Č	č	C	Č	· C	Č	Č	A	A	C
,	1604-2208	9	2014	Č	Č	Č	Č	Č	Č	T	Ĉ	C	Č
20	1604-2208	10	2177	Ť	Ť	T	T	T	T	Ċ	T	T	T
	5748-6485	11	5906	Ĉ	Ť	Ť	Ĉ	Ť	Ť	T	Ċ	T	Ċ
	5748-6485	12	6010	Č	Ĉ	Ĉ	č	Ĉ	Ť	Ť	Č	Ċ	Č
	8035-8653	13	8110	Ğ	Ğ	Ğ	Ğ	Ğ	Ġ	Ġ	Ğ	Ğ	G
	8035-8653	14	8333	č	Č	Č	Č	Č	Č	T	Č	C	C
25	8035-8653	15	8354	Ă	Ă	Ā	Ā	A	A	Ā	G	A	A
	8035-8653	16	8402	A	A	A	A	A	A	G	A	A	A
	8035-8653	17	8459	A	A	A	A	A	A	A	A	A	A
	9942-10628	18	10203	G	G	G	G	G	G	G	G	G	G
	9942-10628	19	10512	T	T	Č	T	T	T.	T	T	T	T
20			10012	•	•	•	•	1		1	1	1	1
30													
30	Region	PS	PS	Iso	gene N	Jumbe	r(đ) (Þ	art 2)					
30	Region Examined(a)	PS No.(b)	PS Position(c)			Jumber			16	17	1 Ř	` 10	20
30	Region Examined(a) 427-1437		Position(c)	11	12	13	14	15	16 G	17 G	18 G	` 19 G	20 G
30	Examined(a) 427-1437	No.(b)	Position(c) 504	11 G	12 G-	13 G	14 G	15 [°] G	G	G	G	G	G
35	Examined(a) 427-1437 427-1437	No.(b) 1 2	Position(c) 504 717	11 G C	12 G- C	13 G C	14 G C	15 G C	G C	G C	G C	G C	G C
	Examined(a) 427-1437 427-1437 427-1437	No.(b) 1 2 3	Position(c) 504 717 744	11 G C G	12 G C G	13 G C G	14 G C G	15 G C G	G C G	G C G	G C G	G C G	G C T
	Examined(a) 427-1437 427-1437 427-1437	No.(b) 1 2 3 4	Position(c) 504 717 744 778	11 G C G T	12 G C G T	13 G C G T	14 G C G T	15 G C G T	G C G T	G C G T	G C G T	G C G T	G C T T
	Examined(a) 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5	Position(c) 504 717 744 778 1009	11 G C G T C	12 G C G T	13 G C G T	14 G C G T	15 G C G T	G C G T G	G C G T G	G C G T G	G C G T G	G C T T G
	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6	Position(c) 504 717 744 778 1009 1045	G C G T C C	12 G C G T C	13 G C G T G	14 G C G T G	15 G C G T G	G C G T G C	G C G T G C	G C G T G C	G C G T G C	G C T T G C
	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6 7	Position(c) 504 717 744 778 1009 1045 1122	II G C G T C G	12 G C G T C C	13 G C G T G C	14 G C G T G C	15 G C G T G C	G C G T G C G	G C G T G C G	G C G T G C G	G C G T G C G	G C T T G C
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437	No.(b) 1 2 3 4 5 6 7 8	Position(c) 504 717 744 778 1009 1045 1122 1218	II G C G T C C G	12 G C G T C C G C	13 G C G T G C G	14 G C G T G C G A	15 G C G T G C G	G C G T G C G C	G C G C C	G C G T G C G C	G C G C C C	G C T T G C G
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208	No.(b) 1 2 3 4 5 6 7 8 9	Position(c) 504 717 744 778 1009 1045 1122 1218 2014	II G C G T C C G C	12 G C G T C C G T	G C G C C G A C	14 G C G T G C G A C	15 G C G T G C G A	G C G T G C G C C	G C G T G C G C	G C G C C	G C G T G C G C C	G C T T G C G C
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208	No.(b) 1 2 3 4 5 6 7 8 9 10	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177	II G C G T C C G C C T	12 G C G T C C G C T C	G C G C G A C T	14 G C G T G C G A C	15 G C G T G C G A C	G C G T G C C T	G C G T G C G C C T	G C G T G C G C C T	G C G C C T	G C T G C G C C T
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485	No.(b) 1 2 3 4 5 6 7 8 9 10 11	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906	II G C G T C C G C C T T	12 G C G T C C G C T C T	G C G C C C T C	14 G C G T G C G A C T T	15 G C G T G C G A C	G C G T G C C T C	G C G T G C C C T T	G C G C C C C T T	G C G C C T T	G C T T G C G C C T T
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010	II G C G T C C G C C T T C	12 G C G T C C G C T C T C	13 G C G T G C G A C T C	14 G C G T G C G A C T T C	15 G C G T G C G A C T T C	G C G T G C G C C T C C	G C G T G C G C C T T C	G C G T G C G C C T T C	G C G T G C C T T C	G C T T G C G C C T T C
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110	II GCGTCCGCCTTCG	12 G C G T C C G C T C T C G	13 G C G T G C G A C T C C A	14 G C G T G C G A C T T C G	15 G C G T G C G A C T T C G	G C G T G C G C C T C C G	G C G T G C G C C T T C A	G C G T G C G C C T T C G	G C G T G C G C C T T C G	G C T T G C G C C T T C G
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333	II GCGTCCGGCTTCGGC	12 G C G T C C G C T C T C G C	13 G C G T G C G A C T C C A C	14 G C G T G C G A C T T C G C	15 G C G T G C G A C T T C G C	GCGTGCGCCTCCGC	G C G T G C C T T C A C	G C G T G C G C C T T C G C	G C G T G C C C T T C G C	G C T T G C G C T T C G C
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354	II G C G T C C G C C T T C G C A	12 G C G T C C G C T C T C G C A	13 G C G T G C G A C T C C A C A	14 G C G T G C G A C T T C G C A	15 G C G T G C G A C T T C G C A	G C G T G C G C C T C C G C A	G C G T G C C T T C A C A	G C G C C T T C G C A	G C G T G C G C T T C G C A	G C T T G C G C C T T C G C A
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	II GCGTCCGCCTTCGGCAA	12 G C G T C C G C T C T C G C A G	13 G C G T G C G A C T C C A C A A	14 GCGTGCGACTTCGCAA	15 GCGTGCGACTTCGCAA	G C G T G C G C C T C C G C A A	G C G T G C C T T C A C A A	G C G T G C C T T C G C A A	G C G T G C C C T T C G C A A	G C T T G C G C C T T C G C A A
35	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402 8459	II G C G T C C G C C T T C G C A A A	12 G C G T C C G C T C T C G C A G C	13 G C G T G C G A C T C C A C A A A	14 GCGTGCGACTTCGCAAA	15 GCGTGCGACTTCGCAAAA	G C G T G C G C C T C C G C A A A	G C G T G C C T T C A C A A A	G C G T G C C T T C G C A A A	G C G T G C G C T T C G C A A A	G C T T G C G C C T T C G C A A A
35 40 45	Examined(a) 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 427-1437 1604-2208 1604-2208 5748-6485 5748-6485 8035-8653 8035-8653 8035-8653	No.(b) 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16	Position(c) 504 717 744 778 1009 1045 1122 1218 2014 2177 5906 6010 8110 8333 8354 8402	II GCGTCCGCCTTCGGCAA	12 G C G T C C G C T C T C G C A G	13 G C G T G C G A C T C C A C A A	14 GCGTGCGACTTCGCAA	15 GCGTGCGACTTCGCAA	G C G T G C G C C T C C G C A A	G C G T G C C T T C A C A A	G C G T G C C T T C G C A A	G C G T G C C C T T C G C A A	G C T T G C G C C T T C G C A A

	Region	PS	PS	Isogene Number(d) (Part 3)		
55	Examined(a)	No.(b)	Position(c)	21	22	:
	427-1437	' 1	504	G	T	
	427-1437	2	717	T	C	
	427-1437	3	744	G	G	
	427-1437	4	<i>77</i> 8	С	T	
60	427-1437	5	1009	C	G	
	427-1437	6	1045	C	C	
	427-1437	7	1122	G	G	
	427-1437	8	1218	C	C	
	1604-2208	9	2014	С	С	
65	1604-2208	10	2177	T	T	•
	5748-6485	11	5906	C	T	
	5748-6485	12	6010	C	C	
	8035-8653	13	8110	G	Α	
	8035-8653	14	8333	C	C	
70	8035-8653	15	8354	Α	Α	•
	8035-8653	16	8402	Α	Α	
	8035-8653	17	8459	Α	Α	
	9942-10628	18	10203	G	G	
	9942-10628	19	10512	T	С	
75					1	1ido mositions d

(a) Region examined represents the nucleotide positions defining the start and stop positions within SEQ ID NO:1 of the regions sequenced;
(b) PS = polymorphic site;
(c) Position of PS within SEQ ID NO:1;
(d) Alleles for TNFRSF11B isogenes are presented 5' to 3' in each column.